

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:11:15 ; Search time 42 Seconds
(without alignments)
166.285 Million cell updates/sec

Title: US09497591-1-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHSLRXRCIXX.....XXAKXIFVDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	182	91.0	419	22	AAE08627 Human protein C de
2	182	91.0	419	22	AAE08628 Human protein C de
3	182	91.0	419	22	AAE08629 Human protein C de
4	182	91.0	419	22	AAE08627 Human protein C de
5	182	91.0	419	22	AAE08627 Human protein C de
6	176	88.0	44	20	AAE08627 Modified GLA domai
7	174	87.0	44	20	AAE08627 Modified GLA domai
8	174	87.0	44	20	AAE08627 Modified GLA domai
9	174	87.0	419	22	AAE08630 Human protein C de

10	174	87.0	419	22	AAE08627	Human protein C de
11	174	87.0	419	22	AAE08627	Human protein C de
12	170	85.0	45	23	ABB79950	Human protein C mu
13	168	84.0	44	20	AAE08627	Modified GLA domai
14	168	84.0	44	20	AAE08627	Modified GLA domai
15	168	84.0	44	20	AAE08627	Human protein C GL
16	168	84.0	44	20	AAE08627	Modified GLA domai
17	168	84.0	44	22	AAE08627	Human protein C ga
18	168	84.0	45	19	AAE08627	Partial human prot
19	168	84.0	45	23	ABB79947	Human protein C GL
20	168	84.0	415	21	AAE08627	Truncated human pr
21	168	84.0	419	14	AAE08627	Protein C (PC). H
22	168	84.0	419	19	AAE08627	Primary structure
23	168	84.0	419	22	AAE08627	Human mature wild
24	168	84.0	419	22	AAE08627	Wild-type human pr
25	168	84.0	419	22	AAE08627	Human protein C de
26	168	84.0	419	22	AAE08627	Human protein C de
27	168	84.0	419	22	AAE08627	Human protein C de
28	168	84.0	419	22	AAE08627	Human protein C de
29	168	84.0	419	23	AAU99002	Human protein C zy
30	168	84.0	419	23	AAU99003	Human protein C zy
31	168	84.0	419	23	AAU99004	Human protein C zy
32	168	84.0	419	23	AAU99005	Human protein C zy
33	168	84.0	419	23	AAU99006	Human protein C zy
34	168	84.0	419	23	AAU99007	Human protein C zy
35	168	84.0	419	23	AAU99008	Human protein C zy
36	168	84.0	419	23	AAU99009	Human protein C zy
37	168	84.0	419	23	AAU99010	Human protein C zy
38	168	84.0	419	23	AAU99011	Human protein C zy
39	168	84.0	419	23	AAU99012	Human protein C zy
40	168	84.0	419	23	AAU99013	Human protein C zy
41	168	84.0	419	23	AAU99014	Human protein C zy
42	168	84.0	419	23	AAU99015	Human protein C zy
43	168	84.0	419	23	AAU99016	Human protein C zy
44	168	84.0	419	23	AAU99017	Human protein C zy
45	168	84.0	419	23	AAU99018	Human protein C zy

ALIGNMENTS

RESULT 1
AAE08627
ID AAE08627 standard; Protein; 419 AA.

XX AC AAE08627;

XX DT 01-NOV-2001 (first entry)

XX DE Human protein C derivative #1.

XX DE Human; protein C derivative; anticoagulation activity; thrombosis;
XX DE serpin inactivation; acute coronary syndrome; myocardial infarction;
XX DE vascular occlusive disorder; hypercoagulable state; angina; sepsis;
XX DE disseminated intravascular coagulation; DIC; burn; transplantation;
XX DE sickle cell disease; viral haemorrhagic fever; protein C deficiency;
XX DE haemolytic uremic syndrome; acute arterial thrombotic occlusion;
XX DE thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.

XX OS Homo sapiens.

XX PN WO200159084-A1.

XX PD 16-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US01221.

XX PR 11-FEB-2000; 2000US-0181948.

XX PR 14-MAR-2000; 2000US-0189199.

XX PA (ELIL) LILLY & CO ELI.

XX PI Gerlitz BE, Grinnell BW, Jones BE;

XX	WPI; 2001-514662/56.	XX	WPI; 2001-514662/56.
DR	N-PSDB; AAD15225.	DR	N-PSDB; AAD15225.
XX		XX	
PT	Protein C derivative for treating acute coronary syndromes, vascular	PT	Protein C derivative for treating acute coronary syndromes, vascular
PT	occlusive disorders, thrombotic disorders and sepsis, comprises	PT	occlusive disorders, thrombotic disorders and sepsis, comprises
PT	substitutions at specified amino acid positions -	PT	substitutions at specified amino acid positions -
XX		XX	
PS	Claim 3; Page 46-47; 59pp; English.	PS	Claim 4; Page 47-48; 59pp; English.
XX		XX	
CC	The invention relates to human protein C derivatives and nucleic acid	CC	The invention relates to human protein C derivatives and nucleic acid
CC	molecules encoding such derivatives. These derivatives have increased	CC	molecules encoding such derivatives. These derivatives have increased
CC	anticoagulation activity, resistance to serpin inactivation and	CC	anticoagulation activity, resistance to serpin inactivation and
CC	increased sensitivity to thrombin activation compared to wild type	CC	increased sensitivity to thrombin activation compared to wild type
CC	protein C, and retains the biological activity of the wild type human	CC	protein C, and retains the biological activity of the wild type human
CC	protein C. Protein C derivatives are useful in the manufacture of a	CC	protein C. Protein C derivatives are useful in the manufacture of a
CC	medicament for the treatment of acute coronary syndromes e.g. myocardial	CC	medicament for the treatment of acute coronary syndromes e.g. myocardial
CC	infarction and unstable angina; and disease states predisposing to	CC	infarction and unstable angina; and disease states predisposing to
CC	thrombosis; vascular occlusive disorders and hypercoagulable states e.g.	CC	thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
CC	disseminated intravascular coagulation (DIC), burns, transplantations,	CC	disseminated intravascular coagulation (DIC), burns, transplantations,
CC	thalassaemia, sickle cell disease, viral haemorrhagic fever and	CC	thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC	haemolytic uremic syndrome; sepsis in combination with bacterial	CC	haemolytic uremic syndrome; sepsis in combination with bacterial
CC	permeability increasing protein; thrombotic disorders in combination	CC	permeability increasing protein; thrombotic disorders in combination
CC	with an anti-platelet agent; protein C deficiency; acute arterial	CC	with an anti-platelet agent; protein C deficiency; acute arterial
CC	thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral	CC	thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
CC	or peripheral arteries or in vascular grafts in combination with a	CC	or peripheral arteries or in vascular grafts in combination with a
CC	thrombolytic agent. Nucleic acid molecules of the invention are useful	CC	thrombolytic agent. Nucleic acid molecules of the invention are useful
CC	for treating humans with genetically predisposed prothrombotic disorders	CC	for treating humans with genetically predisposed prothrombotic disorders
CC	by gene therapy. The present sequence is human protein C derivative.	CC	by gene therapy. The present sequence is human protein C derivative.
XX		XX	
SQ	Sequence 419 AA;	SQ	Sequence 419 AA;
	Query Match 91.0%; Score 182; DB 22; Length 419;		Query Match 91.0%; Score 182; DB 22; Length 419;
	Best Local Similarity 79.5%; Pred. No. 1e-21; Indels 0; Gaps 0;		Best Local Similarity 79.5%; Pred. No. 1e-21; Indels 0; Gaps 0;
	Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;		Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY	1 ANSFLXXLRHGSLSRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44	QY	1 ANSFLXXLRHGSLSRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
DB	1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44	DB	1 ANSFLEELRHGSLERECIEICDFEAKEIFEDVDDTLAFWSKH 44
RESULT 2		RESULT 3	
AAE08628		AAE08629	
ID	AAE08628 standard; Protein; 419 AA.	ID	AAE08629 standard; Protein; 419 AA.
AC	AAE08628;	AC	AAE08629;
XX		XX	
DT	01-NOV-2001 (first entry)	DT	01-NOV-2001 (first entry)
XX		XX	
DE	Human protein C derivative #2.	DE	Human protein C derivative #3.
XX		XX	
KW	Human; protein C derivative; anticoagulation activity; thrombosis;	KW	Human; protein C derivative; anticoagulation activity; thrombosis;
KW	serpin inactivation; acute coronary syndrome; myocardial infarction;	KW	serpin inactivation; acute coronary syndrome; myocardial infarction;
KW	vascular occlusive disorder; hypercoagulable state; angina; sepsis;	KW	vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW	disseminated intravascular coagulation; DIC; burn; transplantation;	KW	disseminated intravascular coagulation; DIC; burn; transplantation;
KW	sickle cell disease; viral haemorrhagic fever; protein C deficiency;	KW	sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW	haemolytic uremic syndrome; acute arterial thrombotic occlusion;	KW	haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW	thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.	KW	thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PH	WO200159084-A1.	PH	WO200159084-A1.
FT	16-AUG-2001.	FT	16-AUG-2001.
XX		XX	
XX	02-FEB-2001; 2001WO-US01221.	XX	02-FEB-2001; 2001WO-US01221.
XX	11-FEB-2000; 2000US-0181948.	XX	11-FEB-2000; 2000US-0181948.
XX	14-MAR-2000; 2000US-0189199.	XX	14-MAR-2000; 2000US-0189199.
XX	(ELIL) LILLY & CO ELI.	XX	(ELIL) LILLY & CO ELI.
XX	Gerlitz BE, Grinnell BW, Jones BE;	XX	Gerlitz BE, Grinnell BW, Jones BE;

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XX WPI; 2001-514662/56.
DR N-PSDB; AAD15226.
XX
XX Protein C derivative for treating acute coronary syndromes, vascular
PT occlusive disorders, thrombotic disorders and sepsis, comprises
PT substitutions at specified amino acid positions -
XX
XX Claim 4; Page 47-48; 59pp; English.
XX
XX The invention relates to human protein C derivatives and nucleic acid
CC molecules encoding such derivatives. These derivatives have increased
CC anticoagulation activity, resistance to serpin inactivation and
CC increased sensitivity to thrombin activation compared to wild type
CC protein C, and retains the biological activity of the wild type human
CC protein C. Protein C derivatives are useful in the manufacture of a
CC medicament for the treatment of acute coronary syndromes e.g. myocardial
CC infarction and unstable angina; and disease states predisposing to
CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
CC disseminated intravascular coagulation (DIC), burns, transplantations,
CC thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC haemolytic uremic syndrome; sepsis in combination with bacterial
CC permeability increasing protein; thrombotic disorders in combination
CC with an anti-platelet agent; protein C deficiency; acute arterial
CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
CC or peripheral arteries or in vascular grafts in combination with a
CC thrombolytic agent. Nucleic acid molecules of the invention are useful
CC for treating humans with genetically predisposed prothrombotic disorders
CC by gene therapy. The present sequence is human protein C derivative.
XX
SQ Sequence 419 AA;
Query Match 91.0%; Score 182; DB 22; Length 419;
Best Local Similarity 79.5%; Pred. No. 1e-21;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps
QY 1 ANSFLXXLRHGLSRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
    ||||| ||||| || ||||| ||||| ||||| |||||
DB 1 ANSFLEELRHGSLERECIEICDFEAKKEIFEDVDDTLAFWSKH 44
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 3
AAE08629
ID AAE08629 standard; Protein; 419 AA.
XX
XX AAE08629;
AC
XX
XX 01-NOV-2001 (first entry)
XX
XX Human protein C derivative #3.
XX
XX Human; protein C derivative; anticoagulation activity; thrombosis;
KW serpin inactivation; acute coronary syndrome; myocardial infarction;
KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW disseminated intravascular coagulation; DIC; burn; transplantation;
KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 10 /note= "Encoded by CAA"
FT
XX
XX WO200159084-A1.
XX
XX 16-AUG-2001-
XX
XX 02-FEB-2001; 2001WO-US01221.
XX
XX 11-FEB-2000; 2000US-0181948.
XX
XX 14-MAR-2000; 2000US-0189199.
XX

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XX PA (BLIL) LILLY & CO ELI.

XX PI Gerlitz BE, Grinnell BW, Jones BE;

XX DR WPI; 2001-514662/56.

XX DR N-PSDB; AAD15227.

XX XX Protein C derivative for treating acute coronary syndromes, vascular

XX PT occlusive disorders, thrombotic disorders and sepsis, comprises

XX PT substitutions at specified amino acid positions -

XX XX Claim 5; Page 48-49; 59pp; English.

XX XX The invention relates to human protein C derivatives and nucleic acid

XX CC molecules encoding such derivatives. These derivatives have increased

XX CC anticoagulation activity, resistance to serpin inactivation and

XX CC increased sensitivity to thrombin activation compared to wild type

XX CC protein C, and retains the biological activity of the wild type human

XX CC protein C. Protein C derivatives are useful in the manufacture of a

XX CC medicament for the treatment of acute coronary syndromes e.g. myocardial

XX CC infarction and unstable angina; and disease states predisposing to

XX CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.

XX CC disseminated intravascular coagulation (DIC), burns, transplantations,

XX CC thalassaemia, sickle cell disease, viral haemorrhagic fever and

XX CC haemolytic uremic syndrome; sepsis in combination with bacterial

XX CC permeability increasing protein; thrombotic disorders in combination

XX CC with an anti-platelet agent; protein C deficiency; acute arterial

XX CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral

XX CC or peripheral arteries or in vascular grafts in combination with a

XX CC thrombolytic agent. Nucleic acid molecules of the invention are useful

XX CC for treating humans with genetically predisposed prothrombotic disorders

XX CC by gene therapy. The present sequence is human protein C derivative.

XX SQ Sequence 419 AA;

Query Match 91.0%; Score 182; DB 22; Length 419;

Best Local Similarity 79.5%; Pred. No. 1e-21;

Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSXRCIXICXICDPXAKXIFEDVDTLAFWSKH 44

DB 1 ANSFLXLRHGSXRCIEICDPFEAKEIFEDVDTLAFWSKH 44

RESULT 4

AAB82675

ID AAB82675 standard; Protein; 419 AA.

XX AC AAB82675;

XX DT 15-OCT-2001 (first entry)

XX DE Human protein C derivative (S1LG/Q32E/N33D/L194S).

XX KW Protein C; human; coronary syndrome; thrombosis; angina;

XX KW myocardial infarction; vascular occlusive disorder;

XX KW hypercoagulation; sepsis; protein C deficiency; occlusion;

XX KW thromboembolism; stenosis; antibacterial; immunosuppressive;

XX KW thrombolytic; cardiac; antianginal; anticoagulant; therapy;

XX KW mutant; mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 11

FT /note= "Ser in wild-type protein"

FT Misc-difference 32

FT /note= "Gln in wild-type protein"

FT Misc-difference 33

FT /note= "Asn in wild-type protein"

FT Misc-difference 194

FT Domain /note= "Leu in wild-type protein"

FT 1..45 /note= "Gla domain"

FT Disulfide-bond 50..69

FT Disulfide-bond 59..84

FT Disulfide-bond 80..89

FT Disulfide-bond 98..109

FT Disulfide-bond 120..133

FT Disulfide-bond 141..277

FT Disulfide-bond 196..212

FT Disulfide-bond 331..345

FT Disulfide-bond 356..384

FT Cleavage-site 156..157

FT /note= "cleavage makes a 2-chain inactive

FT precursor (155-amino acid light chain

FT attached via a disulfide bond to a

FT 262-amino acid heavy chain)"

FT 6 /note= "gamma-carboxylated"

FT Modified-site 7 /note= "gamma-carboxylated"

FT Modified-site 14 /note= "gamma-carboxylated"

FT Modified-site 16 /note= "gamma-carboxylated"

FT Modified-site 19 /note= "gamma-carboxylated"

FT Modified-site 20 /note= "gamma-carboxylated"

FT Modified-site 25 /note= "gamma-carboxylated"

FT Modified-site 26 /note= "gamma-carboxylated"

FT Peptide 158..169 /note= "gamma-carboxylated"

FT /note= "activation peptide; removal activates the

FT 2-chain zymogen"

FT Cleavage-site 169..170 /note= "thrombin cleavage site"

FT Modified-site 29 /note= "N-glycosylated"

FT Modified-site 248 /note= "N-glycosylated"

FT Modified-site 313 /note= "N-glycosylated"

FT Modified-site 329 /note= "N-glycosylated"

XX /note= "N-glycosylated"

PN W0200157193-A2.

XX 09-AUG-2001.

XX 19-JAN-2001; 2001WO-US00020.

XX 02-FEB-2000; 2000US-0179801.

XX 14-MAR-2000; 2000US-0189197.

XX (BLIL) LILLY & CO ELI.

XX Gerlitz BE, Jones BE;

XX WPI; 2001-496919/54.

XX N-PSDB; AAB26363.

XX Novel human protein C derivative for treating, e.g., myocardial

XX infarction, unstable angina, sepsis, thrombotic disorders, acute

XX arterial thrombotic occlusion, and thromboembolism -

XX Claim 3; Page 52-53; 63pp; English.

XX The present sequence is that of a claimed human protein C

XX derivative in which Ser at amino acid position 11 of the mature

XX wild-type protein C sequence (see AAB82673) is substituted with

XX Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and

CC Leu at position 194 with Ser. The protein is an example of protein
 CC C derivatives of the invention that have at least 2 amino acid
 CC substitutions, but which have increased anticoagulant activity and
 CC resistance to inactivation by serpins compared with the wild-type
 CC protein, while retaining the biological activity of the wild-type
 CC protein. A method of producing the derivatives using recombinant
 CC DNA methods is claimed. The protein C derivatives are useful for
 CC treating coronary syndromes and disease states predisposing to
 CC thrombosis (e.g. myocardial infarction and unstable angina),
 CC vascular occlusive disorders and hypercoagulable states, sepsis (in
 CC combination with bactericidal permeability increasing protein or
 CC with tissue factor pathway inhibitor), thrombotic disorders (in
 CC combination with an anti-platelet agent or by local delivery through
 CC an intracoronary catheter), protein C deficiency, acute arterial
 CC thrombotic occlusion, thromboembolism, or stenosis in coronary,
 CC cerebral or peripheral arteries or in vascular grafts. Human
 CC patients with genetically predisposed prothrombotic disorders may
 CC be treated by gene therapy (all claimed).
 XX
 SQ Sequence 419 AA;

Query Match 91.0%; Score 182; DB 22; Length 419;
 Best Local Similarity 79.5%; Pred. No. 1e-21;
 Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGSIXKXICXIXICDPXKXKXIFEDVDITLAFWSKH 44
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 ANSFLSELRHGSLEKICIEICDFEAKKEIFEDVDITLAFWSKH 44

RESULT 5
 AAB82676
 ID AAB82676 standard; Protein; 419 AA.

AC AAB82676;

XX 15-OCT-2001 (first entry)

DE Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).

XX Protein C; human; coronary syndrome; thrombosis; angina;
 KW myocardial infarction; vascular occlusive disorder;
 KW hypercoagulation; sepsis; protein C deficiency; occlusion;
 KW thromboembolism; stenosis; antibacterial; immunosuppressive;
 KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;
 KW mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 11 /note= "Ser in wild-type protein"

FT Misc-difference 32 /note= "Gln in wild-type protein"

FT Misc-difference 33 /note= "Asn in wild-type protein"

FT Misc-difference 194 /note= "Leu in wild-type protein"

FT Misc-difference 254 /note= "Thr in wild-type protein"

FT Domain 1..45 /note= "Gla domain"

FT Disulfide-bond 50..69

FT Disulfide-bond 59..64

FT Disulfide-bond 80..89

FT Disulfide-bond 98..109

FT Disulfide-bond 120..133

FT Disulfide-bond 141..277

FT Disulfide-bond 196..212

FT Disulfide-bond 331..345

FT Disulfide-bond 356..384

FT Cleavage-site 156..157

FT /note= "cleavage makes a 2-chain inactive
 FT precursor (155-amino acid light chain
 FT attached via a disulfide bond to a
 FT 262-amino acid heavy chain)"
 FT
 FT Modified-site 6 /note= "gamma-carboxylated"
 FT Modified-site 7 /note= "gamma-carboxylated"
 FT Modified-site 14 /note= "gamma-carboxylated"
 FT Modified-site 16 /note= "gamma-carboxylated"
 FT Modified-site 19 /note= "gamma-carboxylated"
 FT Modified-site 20 /note= "gamma-carboxylated"
 FT Modified-site 25 /note= "gamma-carboxylated"
 FT Modified-site 26 /note= "gamma-carboxylated"
 FT Peptide 158..169 /note= "gamma-carboxylated"
 FT /note= "activation peptide; removal activates the
 FT 2-chain zymogen"
 FT Cleavage-site 169..170 /note= "thrombin cleavage site"
 FT Modified-site 29 /note= "N-glycosylated"
 FT Modified-site 248 /note= "N-glycosylated"
 FT Modified-site 313 /note= "N-glycosylated"
 FT Modified-site 329 /note= "N-glycosylated"
 FT /note= "N-glycosylated"
 XX WO200157193-A2.
 PN 09-AUG-2001.
 XX 19-JAN-2001; 2001WO-US00020.
 XX 02-FEB-2000; 2000US-0179801.
 PR 14-MAR-2000; 2000US-0189197.
 XX (ELIL) LILLY & CO ELI.
 XX Gerlitz BE, Jones BE;
 XX WPI; 2001-496919/54.
 DR N-PSDB; AAB26364.
 XX Novel human protein C derivative for treating, e.g., myocardial
 PT infarction, unstable angina, sepsis, thrombotic disorders, acute
 PT arterial thrombotic occlusion, and thromboembolism -
 XX Claim 4; Page 53-54; 63pp; English.
 XX The present sequence is that of a claimed human protein C derivative
 CC in which Ser at position 11 of the mature wild-type protein C
 CC sequence (see AAB82673) is substituted with Gly, Gln at position 32
 CC with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser,
 CC and Thr at position 254 with Ser. It is an example of protein C
 CC derivatives of the invention that have at least 2 amino acid
 CC substitutions, but which have increased anticoagulant activity and
 CC resistance to inactivation by serpins compared with the wild-type
 CC protein, while retaining the biological activity of the wild-type
 CC protein. A method of producing the derivatives using recombinant
 CC DNA methods is claimed. The protein C derivatives are useful for
 CC treating coronary syndromes and disease states predisposing to
 CC thrombosis (e.g. myocardial infarction and unstable angina),
 CC vascular occlusive disorders and hypercoagulable states, sepsis (in
 CC combination with bactericidal permeability increasing protein or
 CC with tissue factor pathway inhibitor), thrombotic disorders (in
 CC combination with an anti-platelet agent or by local delivery through

XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX
XX WO9920767-A1.
XX
XX
PD 29-APR-1999.
XX
XX
PF 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU) UNIV MINNESOTA.
PA
XX
XX Nelsestuen GL;
PI
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
PT
XX
XX Claim 9; Page 82; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX
SQ _Sequence 44 AA;
Query Match 87.0%; Score 174; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.9e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
RESULT 9
AAE08630
ID AAE08630 standard; Protein; 419 AA.
XX
XX AAE08630;
AC
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Human protein C derivative #4.
DE
XX
XX Human; protein C derivative; anticoagulation activity; thrombosis;
KW serpin inactivation; acute coronary syndrome; myocardial infarction;
KW vascular occlusive disorder; hypercoagulable state; angina; sepsis;
KW disseminated intravascular coagulation; DIC; burn; transplantation;
KW sickle cell disease; viral haemorrhagic fever; protein C deficiency;
KW haemolytic uremic syndrome; acute arterial thrombotic occlusion;
KW thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200159084-A1.
PN
XX

PD 16-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US01221.
XX
PR 11-FEB-2000; 2000US-0181948.
PR 14-MAR-2000; 2000US-0189199.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Gerlitz BE, Grinnell BW, Jones BE;
PI WPI; 2001-514662/56.
XX DR N-PSDB; AAD15228.
XX
XX Protein C derivative for treating acute coronary syndromes, vascular
PT occlusive disorders, thrombotic disorders and sepsis, comprises
PT substitutions at specified amino acid positions -
XX
XX Claim 6; Page 50-51; 59pp; English.
XX
XX The invention relates to human protein C derivatives and nucleic acid
CC molecules encoding such derivatives. These derivatives have increased
CC anticoagulation activity, resistance to serpin inactivation and
CC increased sensitivity to thrombin activation compared to wild type
CC protein C, and retains the biological activity of the wild type human
CC protein C. Protein C derivatives are useful in the manufacture of a
CC medicament for the treatment of acute coronary syndromes e.g. myocardial
CC infarction and unstable angina, and disease states predisposing to
CC thrombosis; vascular occlusive disorders and hypercoagulable states e.g.
CC disseminated intravascular coagulation (DIC), burns, transplantations,
CC thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC permeability increasing protein; sepsis in combination with bacterial
CC with an anti-platelet agent; protein C deficiency; acute arterial
CC thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
CC or peripheral arteries or in vascular grafts in combination with a
CC thrombolytic agent. Nucleic acid molecules of the invention are useful
CC for treating humans with genetically predisposed prothrombotic disorders
CC by gene therapy. The present sequence is human protein C derivative.
XX
XX
SQ _Sequence 419 AA;
Query Match 87.0%; Score 174; DB 22; Length 419;
Best Local Similarity 77.3%; Pred. No. 2.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLLRHGSLRXRCIXXICDPXXAKXIFEDVDDTLAFWSKH 44
RESULT 10
AAB82677
ID AAB82677 standard; Protein; 419 AA.
XX
XX AAB82677;
AC
XX
XX 15-OCT-2001 (first entry)
DT
XX
XX Human protein C derivative (H100/S11G/Q32E/N33D/L194S).
DE
XX
XX Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulation; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiatic; antianginal; anticoagulant; therapy;
KW mutant; mutein.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 10
FT

FT Misc-difference 11 /note= "His in wild-type protein"

FT Misc-difference 32 /note= "Ser in wild-type protein"

FT Misc-difference 33 /note= "Gln in wild-type protein"

FT Misc-difference 194 /note= "Asn in wild-type protein"

FT Domain 1..45 /note= "Leu in wild-type protein"

FT Disulfide-bond 50..69 /note= "Gla domain"

FT Disulfide-bond 59..64

FT Disulfide-bond 80..89

FT Disulfide-bond 98..109

FT Disulfide-bond 120..133

FT Disulfide-bond 141..277

FT Disulfide-bond 196..212

FT Disulfide-bond 331..345

FT Disulfide-bond 356..384

FT Cleavage-site 156..157

FT /note= "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"

FT Modified-site 6 /note= "gamma-carboxylated"

FT Modified-site 7 /note= "gamma-carboxylated"

FT Modified-site 14 /note= "gamma-carboxylated"

FT Modified-site 16 /note= "gamma-carboxylated"

FT Modified-site 19 /note= "gamma-carboxylated"

FT Modified-site 20 /note= "gamma-carboxylated"

FT Modified-site 25 /note= "gamma-carboxylated"

FT Modified-site 26 /note= "gamma-carboxylated"

FT Peptide 158..169 /note= "activation peptide; removal activates the 2-chain zymogen"

FT Cleavage-site 169..170 /note= "thrombin cleavage site"

FT Modified-site 29 /note= "N-glycosylated"

FT Modified-site 248 /note= "N-glycosylated"

FT Modified-site 313 /note= "N-glycosylated"

FT Modified-site 329 /note= "N-glycosylated"

FT WO200157193-A2.

XX 09-AUG-2001.

XX 19-JAN-2001; 2001WO-US00020.

XX 02-FEB-2000; 2000US-0179801.

PR 14-MAR-2000; 2000US-0189197.

XX (ELIL) LILLY & CO ELI.

XX Gerlitz BE, Jones BE;

PI WPI: 2001-496919/54.

DR N-PSDB; AAH26365.

XX Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute

PT

PT arterial thrombotic occlusion, and thromboembolism -

XX Claim 5; Page 54-55; 63pp; English.

XX The present sequence is that of a claimed human protein C derivative in which His at position 10 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).

XX Sequence 419 AA;

QY 1 ANSFLXLLRHGSLXRCIXXICDPYXAXXIFEDVDDTLAFWSKH 44

DB 1 ANSFLLELRQGSLEECIEICDFEAKEIFEDVDDTLAFWSKH 44

RESULT 11

AAB82678

ID AAB82678 standard; Protein; 419 AA.

XX AAB82678;

XX 15-OCT-2001 (first entry)

DT Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).

DE Protein C; human; coronary syndrome; thrombosis; angina;

XX myocardial infarction; vascular occlusive disorder;

KW hypercoagulation; sepsis; protein C deficiency; occlusion;

KW thromboembolism; stenosis; antibacterial; immunosuppressive;

KW thrombolytic; cardiant; antianginal; anticoagulant; therapy;

KW mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FX Misc-difference 10 /note= "His in wild-type protein"

FT Misc-difference 11 /note= "Ser in wild-type protein"

FT Misc-difference 32 /note= "Gln in wild-type protein"

FT Misc-difference 33 /note= "Asn in wild-type protein"

FT Misc-difference 194 /note= "Leu in wild-type protein"

FT Misc-difference 254 /note= "Thr in wild-type protein"

FT Domain 1..45 /note= "Gla domain"

FT

Query Match 84.0%; Score 168; DB 20; Length 44;
Best Local Similarity 95.5%; Pred. No. 1.9e-20;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ANSFLXXLRHGLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH	44
D _b	1	ANSFLXXLRHGLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH	44

RESULT 15

AAY18303
ID AAY18303 standard; peptide: 44 AA.

AA AAY18303;

17-AUG-1999 (first entry)

Human protein C GLA domain.

GLA domain; vitamin K-dependent protein; clotting disorder;
KW therapy.

xx
OS
Homo sapiens.

AA	FH	Key	Location/Qualifiers

FT	Misc-difference	1.44	
FT			/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT			

PN WO9920767-A1.

29-APR-1999.

20-OCT-1998: 98WO-US22152.

AA
PR 23-OCT-1997; 97US-0955636.

PA (MINU) UNIV MINNESOTA.

PI Nelsestuen GL:

DR WPI; 1999-288309/24.

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders

PS Disclosure; Page 14; 86pp; English.

This sequence is the protein C GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.

Sequence 44 AA;

Query Match	84.0%	Score 168;	DB 20;	Length 44;
Best Local Similarity	93.2%	Pred. No. 1.9e-20;		
Matches 41;	Conservative	2;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy	1	ANSFLXXLRHGS	LXRCIXXCDFXXAKXIFEDVDDTLAFWSKH	44
			:	
Db	1	ANSFLXXLRHSSL	LXRCIXXCDFXXAKXIFONVDTLAFWSKH	44

Search completed: December 30, 2003, 09:18:18
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:16:41 ; Search time 21 Seconds
(without alignments)
201.496 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHGSIXRCIXX.....XXAKXIFdVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	168	84.0	461	1 KXHU	protein C (activat
2	139	69.5	461	1 JX0210	protein C (activat
3	138	69.0	461	1 S18994	protein C (activat
4	121	60.5	456	1 KXBO	coagulation factor
5	113	56.5	482	1 EXRT	coagulation factor
6	109	54.5	492	1 EXBO	coagulation factor
7	108	54.0	488	1 EXHU	coagulation factor
8	100	50.0	443	2 I4932	coagulation factor
9	98	49.0	466	1 KPHU7	coagulation factor
10	84.5	42.2	617	2 S10511	thrombin (EC 3.4.2
11	84.5	42.2	618	2 A35827	thrombin (EC 3.4.2
12	84	42.0	407	1 KFB07	coagulation factor
13	82	41.0	622	1 TBHU	thrombin (EC 3.4.2
14	81	40.5	475	1 EXCH	coagulation factor
15	80	40.0	642	2 S53434	plasma protein S p
16	80	40.0	676	1 KXHUS	plasma protein S p
17	79	39.5	452	1 A30351	coagulation factor
18	79	39.5	459	2 JQ0419	coagulation factor
19	79	39.5	646	2 S38919	plasma protein S -
20	78	39.0	675	1 KXBOS	plasma protein S p
21	76	38.0	675	1 KXRTS	plasma protein S p
22	75	37.5	641	1 KFHU	coagulation factor
23	73	36.5	642	2 S53433	plasma protein S p
24	72	36.0	416	1 KFB0	coagulation factor
25	70	35.0	625	1 TBBO	thrombin (EC 3.4.2
26	69	34.5	675	1 KXMS	plasma protein S p
27	67.5	33.8	396	1 KXBOZ	plasma protein 2 -
28	63.5	31.8	422	1 KKHUZ	plasma protein 2 p
29	60	30.0	673	2 A48089	growth arrest-spec

ALIGNMENTS

RESULT 1

KXHU

protein C (activated) (EC 3.4.21.69) precursor - human
N:Alternate names: autoprothrombin IIA; plasma protein C
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
A:Accession: A22331; A25426; A21781; A23789; A00927
R:Poster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A:Title: The nucleotide sequence of the gene for human protein C.
A:Reference number: A22331; MUID:85270390; PMID:2991887
A:Accession: A22331
A:Molecule type: DNA
A:Residues: 1-461 <POS1>
A:Cross-references: GB:M1128; NID:g190333; PIDN:AAA60166.1; PID:g190334
R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A:Title: Evolution and organization of the human protein C gene.
A:Reference number: A25426; MUID:86120978; PMID:3511471
A:Accession: A25426
A:Molecule type: DNA
A:Residues: 1-445, 'L', 446-461 <PLU>
A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
R:Poster, D.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A:Title: Characterization of a cDNA coding for human protein C.
A:Reference number: A21781; MUID:84272714; PMID:6589623
A:Accession: A21781
A:Molecule type: mRNA
A:Residues: 'O', 107-461 <POS2>
A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
R:Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
A:Title: The structure and evolution of a 461 amino acid human protein C precursor and it
A:Reference number: A23789; MUID:85269639; PMID:2991859
A:Accession: A23789
A:Molecule type: mRNA
A:Residues: 1-461 <BEC>
A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA36528.1; PID:g763120
R:Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 265, 11397-11404, 1990
A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
A:Reference number: A44605; MUID:90293094; PMID:1694179
A:Contents: annotation; carbohydrate binding sites; activation peptide
A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
R:Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor
A:Reference number: A44606; MUID:92184750; PMID:1544894
A:Contents: annotation; beta-hydroxyaspartic acid
C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
ivation of factor Va is strongly enhanced by complexing with protein S. Protein C also fa

growth potentiatin
growth arrest-spec
probable MAP kinase
probable MAP kinase
probable MAP kinase
probable MAP kinase
hypothetical prote
hypothetical prote
alcohol dehydrogen
primosomal replica
protein-tyrosine k
hypothetical prote
hypothetical prote
ammonium transport
VSG expression sit
protein-tyrosine k
tyrosine kinase re

J. Biol. Chem. 257, 12170-12179, 1982
A;Title: Amino acid sequence of the light chain of bovine protein C.
A;Reference number: A18385; MUID:83007325; PMID:6896876
A;Accession: A18385
A;Molecule type: protein
A;Residues: 40-194 <PER>
A;Note: 82-Lys was also found
R;Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
A;Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
A;Reference number: A19316; MUID:83189769; PMID:6572939
A;Contents: annotation; revision to residue 110
R;Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A;Title: Amino acid sequence of the heavy chain of bovine protein C.
A;Reference number: A18386; MUID:83007326; PMID:6896877
A;Accession: A18386
A;Molecule type: protein
A;Residues: 197-454, 'FV' <STE>
R;Esmon, N.L.; DeBault, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless P
A;Reference number: A37541; MUID:83213513; PMID:6304092
A;Contents: annotation; activation; calcium binding
R;Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A;Title: Structural changes required for activation of protein C are induced by Ca2+ bin
A;Reference number: A37542; MUID:83213514; PMID:6406503
A;Contents: annotation; activation; calcium binding
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
B.
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reacti
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
cognition of the thrombin-thrombomodulin complex.
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;1-29/Domain: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F;24-83/Domain: Gla domain homology <GLA>
F;30-38/Domain: propeptide #status predicted <PRO>
F;40-194/Product: protein C light chain #status experimental <LCH>
F;98-128/Domain: EGF homology <EG1>
F;137-172/Domain: EGF homology <EG2>
F;197-456/Product: protein C heavy chain #status experimental <HCH>
F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat
F;136,289,350/Binding site: carboxylate (Asn) (covalent) #status predicted
F;252,298,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 60.5%; Score 121; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 1.6e-11;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ANSFLXLRGSLRXRCIXXICDPFXKXIFEDVDDTLAFWS 42
Db 40 ANSFLRLPGNVERECSEVCEFEAREIFQNTEDTMFWS 81
RESULT 5
EXRT
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
R;Accession: S49075; JC4670; PS0191; PS0190; I62745
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra
A;Reference number: A58498; MUID:96093366; PMID:8578539

A;Accession: S49075
A;Molecule type: mRNA
A;Residues: 1-482 <STAL>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Note: submitted to the EMBL Data Library, June 1994
R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
A;Accession: JC4670
A;Molecule type: mRNA
A;Residues: 1-482 <STA2>
A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A;Experimental source: Cos-1 cell
R;Enjiyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
A;Reference number: PS0190; MUID:92041742; PMID:1718949
A;Accession: PS0191
A;Molecule type: protein
A;Residues: 41-58, 'X', 60-65 <ENJ1>
A;Accession: PS0190
A;Molecule type: protein
A;Residues: 183-186, 'X', 188-207 <ENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of t
A;Reference number: I46196; MUID:94222160; PMID:8168596
A;Accession: I62745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 295-383, 'G', 385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F;232-482/Product: activation peptide #status predicted <APT>
F;232-460/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;187/Binding site: carboxylate (Asn) (covalent) #status experimental
F;208/Binding site: carboxylate (Thr) (covalent) #status predicted
F;218/Binding site: carboxylate (Asn) (covalent) #status predicted
F;231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
F;274,320,417/Active site: His, Asp, Ser #status predicted
Query Match 56.5%; Score 113; DB 1; Length 482;
Best Local Similarity 43.2%; Pred. No. 3.4e-10;
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
Qy 1 ANSFLXLRGSLRXRCIXXICDPFXKXIFEDVDDTLAFWSKH 44
Db 41 ANSFPEIKKGNLRECEVEICSEFEAREVFEEDNEKTEFPWNY 84
RESULT 6
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N;Alternate names: Stuart factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

A:Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336
 F:199,211/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:221,231/Binding site: carbohydrate (Thr) (covalent) #status experimental
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A:Title: Characterization of an almost full-length cDNA coding for human blood coagulation factor VIIa
 A:Reference number: A22208; MUID:85116545; PMID:2582420
 A:Accession: A22208
 A:Molecule type: mRNA
 A:Residues: 13-441; S', 443-488 <FUN>
 A:Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
 R:Levtus, S.P.; Chung, D.W.; Kistel, W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984
 A:Title: Characterization of a cDNA coding for human factor X
 A:Reference number: A21284; MUID:84222026; PMID:6587384
 A:Accession: A21284
 A:Molecule type: mRNA
 A:Residues: 13-284, 'E', 289-488 <LE2>
 A:Cross-references: GB:K01886
 R:McMullen, B.A.; Fujikawa, K.; Kistel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weiss
 Biochemistry 22, 2875-2884, 1983
 A:Title: Complete amino acid sequence of the light chain of human blood coagulation factor VIIa
 A:Reference number: A20362; MUID:83257207; PMID:6871167
 A:Accession: A20362
 A:Molecule type: protein
 A:Residues: 41-179 <MCW>
 R:Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of human factor VIIa
 A:Reference number: S39414; MUID:94062825; PMID:8243461
 A:Accession: S39415
 A:Molecule type: protein
 A:Residues: 183-234 <INO>
 A:Note: Glycosylation sites
 A:Note: Identification and characterization of beta-hydroxyaspartic acid
 R:Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamesabushanam, K.; Lyman, G.
 Gene 84, 517-519, 1989
 A:Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor VIIa
 A:Reference number: I54051; MUID:90128299; PMID:2612918
 A:Accession: I54051
 A>Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23 <RES>
 A:Cross-references: GB:M32297; NID:g183860; PIDN:AAA52636.1; PID:g553330
 R:Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blumberg, P.M.
 J. Mol. Biol. 232, 947-966, 1993
 A:Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A:Reference number: A49458; MUID:93360277; PMID:8355279
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 C:Comment: The two chains held together by one disulfide bond are formed from a single-coding sequence
 C:Note: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa
 C:Genetics:
 A:Gene: GDB:F10
 A:Cross-references: GDB:119890; OMIM:227600
 A:Map position: 13q34-13q34
 A:Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A:Note: deficiency of this factor causes Stuart disease
 C:Function:
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V
 A:Pathway: blood coagulation
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:11-179/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EGF>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <APT>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental
 F:276,322,419/Active site: His, Asp, Ser #status experimental
 Query Match 54.0%; Score 108; DB 1; Length 488;
 Best Local Similarity 43.2%; Pred. No. 2.2e-09;
 Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ANSFLLXLRHGSLSXRCXXICDPFXAXKXIFEDVDVDTLAFWSKH 44
 DB 41 ANSFLEEMKKGHLERECEETCSYBEAREVFPDSKTFNFWNKY 84
 RESULT 8
 I46932
 coagulation factor VII - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C:Accession: I46932
 R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A:Reference number: I46932; MUID:93190306; PMID:8383365
 A:Accession: I46932
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-443 <BRO>
 A:Cross-references: GB:S56300; NID:g266294; PID:g266295
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F:24-83/Domain: Gla domain homology <GLA>
 F:89-120/Domain: EGF homology <EG1>
 F:130-166/Domain: EGF homology <EG2>
 F:192-425/Domain: trypsin homology <TRY>
 Query Match 50.0%; Score 100; DB 2; Length 443;
 Best Local Similarity 46.3%; Pred. No. 3.9e-08;
 Matches 19; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ANSFLLXLRHGSLSXRCXXICDPFXAXKXIFEDVDVDTLAFW 41
 DB 40 ANSFLEELRPGSLERECEELCSFEAREVFPQSTERTKQFW 80
 RESULT 9
 KFHU7
 coagulation factor VIIa (BC 3.4.21.21) precursor [validated] - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 08-Dec-2000
 C:Accession: A28322; A23819; A31186; B31186; S63524
 R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murray, R.; Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
 A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein
 A:Reference number: A28322; MUID:87260948; PMID:3037537
 A:Accession: A28322
 A:Molecule type: DNA
 A:Residues: 1-466 <OHA>
 A:Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
 R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.
 Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
 A:Title: Characterization of a cDNA coding for human factor VII
 A:Reference number: A23819; MUID:86205965; PMID:3486420
 A:Accession: A23819
 A:Molecule type: mRNA
 A:Residues: 1-466 <HAG>
 A:Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801
 R:Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.A.
 Biochemistry 27, 7785-7793, 1988
 A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a
 A:Reference number: A90539; MUID:89088153; PMID:3264725
 A:Accession: A31186
 A:Molecule type: protein

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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:11:16 ; Search time 12 seconds
(without alignments)
172.431 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHSLRXRCIXX.....XXAKXIFedVDDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	168	84.0	461	1	PRTC_HUMAN
2	139	69.5	461	1	PRTC_MOUSE
3	138	69.0	461	1	PRTC_RAT
4	137	68.5	458	1	PRTC_RABIT
5	122	61.0	459	1	PRTC_PIG
6	121	60.5	456	1	PRTC_BOVIN
7	109	54.5	432	1	FA10_BOVIN
8	108	54.0	488	1	FA10_HUMAN
9	102	51.0	231	1	TMG3_HUMAN
10	101	50.5	490	1	FA10_RABIT
11	100	50.0	444	1	FA7_RABIT
12	98	49.0	466	1	FA7_HUMAN
13	87	43.5	218	1	TMG1_HUMAN
14	84.5	42.2	617	1	THRB_RAT
15	84.5	42.2	618	1	THRB_MOUSE
16	84	42.0	226	1	TMG4_HUMAN
17	84	42.0	407	1	FA7_BOVIN
18	82	41.0	522	1	THRE_HUMAN
19	81	40.5	376	1	FA10_TROCA
20	81	40.5	475	1	FA10_CHICK
21	80	40.0	649	1	PRTS_MACMU
22	80	40.0	676	1	PRTS_HUMAN
23	79	39.5	446	1	FA7_MOUSE
24	79	39.5	452	1	FA9_CANFA
25	79	39.5	459	1	FA9_MOUSE
26	79	39.5	646	1	PRTS_RABIT
27	78	39.0	675	1	PRTS_BOVIN
28	76	38.0	675	1	PRTS_RAT
29	75	37.5	461	1	FA9_HUMAN
30	72	36.0	416	1	FA9_BOVIN
31	70	35.0	625	1	THRB_BOVIN
32	69	34.5	675	1	PRTS_MOUSE
33	67.5	33.8	396	1	PRTC_BOVIN

RESULT 1

ID	PRTC_HUMAN	STANDARD;	PRT;	461 AA.
AC	P04070; Q15189; Q15190; Q16001;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-NOV-1986 (Rel. 03, Last sequence update)			
DE	Vitamin-K-dependent protein C precursor (EC 3.4.21.69)			
DE	(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).			
GN	PROC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85270390; PubMed=2991887;			
RA	Foster D.C., Yoshitake S., Davie E.W.;			
RT	"The nucleotide sequence of the gene for human protein C.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85269639; PubMed=2991859;			
RA	Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,			
RA	Long G.L.;			
RT	"The structure and evolution of a 461 amino acid human protein C			
RT	precursor and its messenger RNA, based upon the DNA sequence of			
RT	cloned human liver cDNAs.";			
RL	Nucleic Acids Res. 13:5233-5247(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86120978; PubMed=3511471;			
RA	Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;			
RT	"Evolution and organization of the human protein C gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,			
RA	Nickerson D.A.;			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 106-461 FROM N.A.			
RX	MEDLINE=84272714; PubMed=6589623;			
RA	Foster D.C., Davie E.W.;			
RT	"Characterization of a cDNA coding for human protein C.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITE ASN-371.			
RX	MEDLINE=90293094; PubMed=1694179;			
RA	Miletich J.P., Broze G.J. Jr.;			
RT	"Beta protein C is not glycosylated at asparagine 329. The rate of			
RT	translation may influence the frequency of usage at asparagine-X-			
RT	cysteine sites.";			
RL	J. Biol. Chem. 265:11397-11404(1990).			
RN	[7]			

O14669 homo sapien
P22891 homo sapien
P43068 candida alb
Q9h270 homo sapien
Q9l866 mus musculus
Q00593 pseudomonas
P44647 haemophilus
P35917 mus musculus
Q26721 trypanosoma
P35916 homo sapien
Q9Y493 homo sapien
P04390 escherichia

ALIGNMENTS

RP HYDROXYLATION.
 RX MEDLINE=92184750; PubMed=1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RT domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 RN [8]
 RP 3D-STRUCTURE MODELING OF 175-450.
 RX MEDLINE=94272342; PubMed=8003977;
 RA Fisher C.L., Greengard J.S., Griffin J.H.;
 RT "Models of the serine protease domain of the human antithrombotic
 RT plasma factor activated protein C and its zymogen.";
 RL Protein Sci. 3:588-599(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
 RX MEDLINE=97157472; PubMed=9003757;
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmen C.,
 RA Bode W.;
 RT "The 2.8 A crystal structure of Gla-domainless activated protein C.";
 RL ENBO J. 15:6822-6831(1996).
 RN [10]
 RP REVIEW ON PROC VARIANTS.
 RX MEDLINE=93190290; PubMed=8446940;
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
 RA Sala N., Cooper D.N.;
 RT "Protein C deficiency: a database of mutations. For the Protein C & S
 RT Subcommittee of the Scientific and Standardization Committee of the
 RT International Society on Thrombosis and Haemostasis.";
 RL Thromb. Haemost. 69:77-84(1993).
 RN [11]
 RP VARIANT CYS-444.
 RX MEDLINE=92204221; PubMed=2437584;
 RA Romeo G., Hassan H.J., Staemfli S., Roncuzzi L., Cianetti L.,
 RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
 RA Cortese R.;
 RT "Hereditary thrombophilia: identification of nonsense and missense
 RT mutations in the protein C gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
 RN [12]
 RP VARIANT TRP-211 (LONDON-1).
 RX MEDLINE=90098906; PubMed=2602169;
 RA Grundy C.B., Chitollie A., Talbot S., Bevan D., Kakkar V.V.,
 RA Cooper D.N.;
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
 RT the protein C gene causing thrombosis.";
 RL Nucleic Acids Res. 17:10513-10513(1989).
 RN [13]
 RP VARIANT CYS-272.
 RX MEDLINE=91329836; PubMed=1868249;
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with
 RT symptomatic protein C deficiency type I: heterogeneity and founder
 RT effects.";
 RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Bovill E.G., Tomczak J.A., Grant B., Bhushan P., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein C Vermont: symptomatic type II protein C deficiency
 RT associated with two GLA domain mutations.";
 RL Blood 79:1456-1465(1992).
 RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Sugahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;

RA Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandrille S., Vidaud M., Aïach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsushita T., Suglura I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gandrille S., Alhenc-Gelas M., Gaussem P., Aillaud M.-F., Dupuy E.,
 RA Juhan-Vague I., Aïach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385;
 RP THR-388 AND VAL-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Gla domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous
 RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS ARG-145; LEU-210; TRP-211; THR-243; LEU-321; MET-340 AND
 RP TYR-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koerber M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with
 RT symptomatic type I protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patraccchini P., Gemmati D., Castaman G., Rodeghiero F.,
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]

FT DISULFID 373 387 BY SIMILARITY.
 FT DISULFID 398 426 BY SIMILARITY.
 FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 51912 MW; 844CF93664EDACD5 CRC64;

Query Match 69.0%; Score 138; DB 1; Length 461;
 Best Local Similarity 59.1%; Pred. No. 8.7e-16;
 Matches 26; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANSELXLRGLSLRXICIXICDPKXAKXIPEDVDDTLAFWSKH 44
 Db 42 ANSFLFVRLSGLEECMBECIDCFEAEQIFQNVEDTLAFWKY 85

RESULT 4

PTC_RABIT STANDARD; PRT; 458 AA.

AC Q28661;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
 GN PROC.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Shen L., He X., Dahlback B.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIA.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
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 CC -----
 CC EMBL; U49933; AAA2956.1; -;
 CC DR HSSP; P04070; 1PCU.
 CC MEROPS; S01.218; -;
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA_Blood.

DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gls_1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF_2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Glycoprotein; Serine protease;
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 27 BY SIMILARITY.
 FT PROPEP 28 36 BY SIMILARITY.
 FT CHAIN 37 458 VITAMIN K-DEPENDENT PROTEIN C.
 FT CHAIN 37 192 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
 FT CHAIN 195 458 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
 FT PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT SITE 209 210 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT DOMAIN 91 126 EGF-LIKE 1.
 FT DOMAIN 130 170 EGF-LIKE 2.
 FT DOMAIN 210 458 SERINE PROTEASE.
 FT MOD_RES 42 42 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 43 43 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 52 52 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 62 62 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
 FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
 FT ACT_SITE 250 250 CHARGE RELAY SYSTEM.
 FT ACT_SITE 296 296 CHARGE RELAY SYSTEM.
 FT ACT_SITE 399 399 CHARGE RELAY SYSTEM.
 FT DISULFID 53 58 BY SIMILARITY.
 FT DISULFID 85 105 BY SIMILARITY.
 FT DISULFID 95 100 BY SIMILARITY.
 FT DISULFID 99 114 BY SIMILARITY.
 FT DISULFID 116 125 BY SIMILARITY.
 FT DISULFID 134 145 BY SIMILARITY.
 FT DISULFID 141 154 BY SIMILARITY.
 FT DISULFID 156 169 BY SIMILARITY.
 FT DISULFID 177 316 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 235 251 BY SIMILARITY.
 FT DISULFID 370 384 BY SIMILARITY.
 FT DISULFID 395 423 BY SIMILARITY.
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 458 AA; 51087 MW; D75A5F90C8F29D7 CRC64;

Query Match

68.5%; Score 137; DB 1; Length 458;

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Best Local Similarity 59.1%; Pred. No. 1.3e-15;
Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANSLFLXRLGSLXRCIXIXICDFXAKXIFEDVDDTLAFWSKH 44
Db 37 ANSFLELRPSLRECEVVECDLEAKEIFQSDVDDTLAFWYK 80

RESULT 5
PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV)
GN PROC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21121490; PubMed=11229814;
RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
RA Kim H.K.W.;
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modeling of membrane binding sites and comparative anatomy of
RT domains."
RL Cell. Mol. Life Sci. 58:148-159(2001).
CC -I- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -I- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -I- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC site is necessary for the recognition of the
CC thrombin-thrombomodulin complex.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF191307; AAC28380.1;
CC HSP: P04070; lPCU.
CC MEROPS: S01.218;
CC InterPro: IPR000152; Asx_hydroxyl.
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR001881; EGF Ca.
CC InterPro: IPR006209; EGF-like.
CC InterPro: IPR002383; GLA_blood.
CC InterPro: IPR006210; IEGF.
CC InterPro: IPR001254; Ser_protease_Try.
CC InterPro: IPR000294; VitK_dep_GLA.

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DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 41 BY SIMILARITY.
FT CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY
FT CHAIN 199 459 PROTEIN C HEAVY CHAIN (BY
FT PEPTIDE 199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 213 214 CLEAVAGE (BY THROMBIN) (BY
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT MOD_RES 214 459 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

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Query Match 61.0%; Score 122; DB 1; Length 459;
Best Local Similarity 52.3%; Pred. No. 4.8e-13;


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FT ACT SITE 397 397 CHARGE RELAY SYSTEM.
FT DISULFID 56 61 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 98 103 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 119 128 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT DISULFID 144 157 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 180 318 INTERCHAIN.
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .).
FT VARIANT 82 82 F -> K.
FT CONFLICT 455 456 VP -> PV (IN REF. 4).
SQ SEQUENCE 456 AA; 51407 MW; CAA6833F894C209 CRC64;

Query Match 60.5%; Score 121; DB 1; Length 456;
Best Local Similarity 50.0%; Pred. No. 7.1e-13;
Matches 21; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ANSFLXLRHGSXRCIXXICDPXXAKXIFEDVDVDTLAFWS 42
Db 40 ANSFLEELRPNVERCESEVCFEAREIFQNTEDTMAFWS 81

RESULT 7
FA10_BOVIN STANDARD; PRT; 492 AA.
AC P00743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;
RT "Amino acid sequence of the light chain of bovine factor X1 (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kistel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1053093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor X1 (Stuart factor): amino-acid sequence of heavy
RT chain.";
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RL J. Mol. Biol. 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
 RA Drakenberg T.;
 RA "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII";
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RA "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male";
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodorigo G., Caonato A., Girolami A., Bernardi F.;
 RA "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7)".
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=9364544;
 RA Marchetti G., Ferrari M., Patraccchini P., Redaelli R., Bernardi F.;
 RA "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kembell-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RA "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=8204879;
 RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RA "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor";
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Caetaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RA "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro)";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [17]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohiwa M., Hayaishi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RA "Factor VII MIE: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain";
 RL Thromb. Haemost. 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RA "A Thr359Met mutation in factor VII of a patient with a hereditary

RT deficiency causes defective secretion of the molecule";
 RL Blood 87:5085-5094(1996).
 RN [19]
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Caetaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RA "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency";
 RL Hum. Mutat. 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
 RA Zaizov R., Seligsohn U.;
 RA "Ala244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews";
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=98235713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.;
 RA "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency";
 RL Br. J. Haematol. 101:47-49(1998).
 RN [22]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
 RA "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN [23]
 RP VARIANTS ASP-295 AND GLN-413
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RA "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes";
 RL Nat. Genet. 22:231-238(1999).
 QY Query Match 49.0%; Score 98; DB 1; Length 466;
 Best Local Similarity 48.8%; Pred. No. 6.4e-09;
 Matches 20; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
 DB 1 ANSFLXXLRHGSIXXICIXXICDXXAKXIFEDVDTLAPW 41
 ||:| | | | | | | | | | | | | | | | | | | | |
 61 ANAFLELRPGSLERECKEQQSFEEARIFDKAERTKLFW 101
 RESULT 13
 TMGL_HUMAN STANDARD; PRT; 218 AA.
 ID TMGL_HUMAN
 AC 014668;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 DE 1).
 GN PRG1 OR TMG1 OR PRGP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404347; PubMed=9256434;

RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 RT gamma-carboxyglutamic acid proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
 CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
 CC -1- PTM: Gla residues are produced after subsequent posttranslational
 CC modifications of glutamic acid by a vitamin K-dependent gamma-
 CC carboxylase.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF009242; AAB67070.1; -;
 DR HSSP; P00740; 1CFH.
 DR Genew; HGNC:9469; PRRG1.
 DR MIM; 604428; -;
 DR GO; GO:0005887; C-integral to plasma membrane; TAS.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR "Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
 FT PROPEP 1 20 POTENTIAL.
 FT CHAIN 21 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
 FT DOMAIN 21 83 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 84 106 POTENTIAL.
 FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 24 61 GLA-RICH.
 FT DOMAIN 131 135 POLY-PRO.
 SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
 Query Match 43.5%; Score 87; DB 1; Length 218;
 Best Local Similarity 36.4%; Pred. No. 2.1e-07;
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 QY 1 ANSFLXLRHGSILRXICXXICDFXAKXIFEDVDITLAFWSKH 44
 Db 21 ANGFFFEIRQSNIERCKEFCFTFEAREAFENNEKTKFWSY 64
 RESULT 14
 ID THRB RAT STANDARD; PRT; 617 AA.
 AC P18292;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 GN P2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=90332426; PubMed=2377469;
 RA Dhanich M., Monard D.;
 RT "cDNA sequence of rat prothrombin.";
 RL Nucleic Acids Res. 18:4251-4251(1990).
 RN [2]
 RP SEQUENCE OF 383-617 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92212913; PubMed=1557383;
 RA Banfield D.K., Macgillivray R.T.;

RT "Partial characterization of vertebrate prothrombin cDNAs:
 RT amplification and sequence analysis of the B chain of thrombin from
 RT nine different species.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
 CC -1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS
 CC FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg|-Gly; activates
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC -1- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC -1- MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 kringle domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X52835; CAA37017.1; -;
 DR EMBL; M81397; AAA42240.1; -;
 DR PIR; S10511; S10511.
 DR HSSP; P00734; IUVS.
 DR MEROPS; S01.217; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003966; Prothrombin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00021; KRINGLE 1; 2.
 DR PROSITE; PS00070; KRINGLE 2; 2.
 DR PROSITE; PS50070; KRINGLE 2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
 KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
 KW Hydrolase; Serine protease; Kringle; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 43
 FT CHAIN 44 617 PROTHROMBIN.
 FT PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).
 FT PEPTIDE 201 323 ACTIVATION PEPTIDE (FRAGMENT 2).
 FT CHAIN 324 359 THROMBIN LIGHT CHAIN (A).

Search completed: December 30, 2003, 09:18:42
Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:16:11 ; Search time 34 Seconds
(without alignments)
333.950 Million cell updates/sec

Title: US09497591-LEDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHGLRXCIXX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	75.0	456	Q9TTR0	Q9TTR0 canis famil
2	139	69.5	460	Q9IWN8	Q9IWN8 mus musculu
3	133	66.5	460	Q99PC6	Q99PC6 mus musculu
4	126	63.0	55	Q8J002	Q8J002 homo sapien
5	126	63.0	55	Q8IXB5	Q8IXB5 homo sapien
6	113	56.5	482	Q63207	Q63207 rattus norv
7	102.5	51.2	443	Q8JHC9	Q8JHC9 brachydanio
8	102	51.0	231	Q8N2N6	Q8N2N6 homo sapien
9	99	49.5	481	Q54740	Q54740 mus musculu
10	99	49.5	481	Q99L32	Q99L32 mus musculu
11	99	49.5	481	Q8B947	Q8B947 mus musculu
12	98	49.0	701	Q96PQ8	Q96PQ8 homo sapien
13	95	47.5	474	Q8JHC8	Q8JHC8 brachydanio
14	93	46.5	469	Q9GMD9	Q9GMD9 ornithorhyn
15	88	44.0	229	Q8JJ40	Q8JJ40 xenopus lae
16	87	43.5	268	Q8NEK6	Q8NEK6 homo sapien

17	83	41.5	376	13	P83370	P83370 hoplocephal
18	82	41.0	100	4	Q15253	Q15253 homo sapien
19	80	40.0	650	4	Q16519	Q16519 homo sapien
20	80	40.0	650	4	Q9NSD0	Q9NSD0 homo sapien
21	79	39.5	446	11	Q81109	Q81109 mus musculu
22	77.5	38.8	542	5	Q8T613	Q8T613 halocynthia
23	77	38.5	138	6	Q28994	Q28994 sus scrofa
24	76	38.0	607	13	Q91001	Q91001 gallus gall
25	75	37.5	446	11	Q8K3U6	Q8K3U6 rattus norv
26	75	37.5	456	4	Q14316	Q14316 homo sapien
27	75	37.5	461	6	Q95ND7	Q95ND7 pan troglod
28	75	37.5	461	6	Q95ND6	Q95ND6 pan troglod
29	73	36.5	648	6	Q29094	Q29094 sus scrofa
30	72.5	36.2	433	13	Q8JHD0	Q8JHD0 brachydanio
31	72.5	36.2	433	13	Q90YK1	Q90YK1 brachydanio
32	72	36.0	49	6	Q95ME8	Q95ME8 bos taurus
33	72	36.0	52	4	Q8IXD5	Q8IXD5 homo sapien
34	71	35.5	98	13	P82807	P82807 notechis sc
35	70	35.0	608	13	Q9PTW7	Q9PTW7 struthio ca
36	69	34.5	52	4	Q8IXC5	Q8IXC5 homo sapien
37	68	34.0	241	11	Q8CI01	Q8CI01 mus musculu
38	68	34.0	399	11	Q9CQW3	Q9CQW3 mus musculu
39	66	33.0	226	11	Q8BM25	Q8BM25 mus musculu
40	66	33.0	226	11	Q8BGN6	Q8BGN6 mus musculu
41	64	32.0	25	11	Q9QVH6	Q9QVH6 rattus sp.
42	64	32.0	179	4	Q8TAS3	Q8TAS3 homo sapien
43	64	32.0	198	11	Q8R1B2	Q8R1B2 mus musculu
44	63	31.5	503	13	Q8AYE4	Q8AYE4 brachydanio
45	60	30.0	673	11	Q61592	Q61592 mus musculu

ALIGNMENTS

RESULT 1

Q9TTR0	PRELIMINARY;	PRT;	456 AA.
ID	Q9TTR0		
AC	Q9TTR0;		
DC	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DE	01-MAR-2003 (Tremblrel. 23, Last annotation update)		
DE	Protein C precursor.		
GN	PROC.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg L.,		
RA	Brenig B.,		
RT	"Molecular characterization and chromosomal assignment of the canine		
RL	protein C gene."		
RL	Mamm. Genome 10:135-139(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-99371952; PubMed-10443005;		
RA	Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;		
RT	"Analysis of canine protein C gene polymorphisms."		
CC	Anim. Genet. 30:237-238(1999).		
RL	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL; AJ001979; CAA05126.1; -		
DR	HSSP; P04070; 1AUT.		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR001881; EGF Ca.		
DR	InterPro; IPR006209; EGF like.		
DR	InterPro; IPR002383; GLA_blood.		
DR	InterPro; IPR006210; IEGF.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	InterPro; IPR000294; VitK_dep_GLA.		
DR	Pfam; PF00008; EGF; 2.		
DR	Pfam; PF00594; gla; 1.		


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Q8J002
ID Q8J002 PRELIMINARY; PRT; 55 AA.
AC Q8J002;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kinoshita S., Iida H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
RA Ono M., Dongchon K., Hamaeaki N.;
RT "Gene Analysis of Anticoagulation Factors in Japanese Thrombotic
RT Patients. Genetic Background of Thrombophilia in Japan.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083700; BAC21172.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6527 MW; 4F89496534A78836 CRC64;

Query Match 63.0%; Score 126; DB 4; Length 55;
Best Local Similarity 67.6%; Pred. No. 1e-13;
Matches 25; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDT 37
DB 19 ANSFLKLRHSSLERECIEICDFEAKEIFQNVDDT 55

RESULT 5
Q8IXB5 PRELIMINARY; PRT; 55 AA.
AC Q8IXB5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein C (Fragment).
GN PROC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,
RA Kurihara M., Wada Y., Ono M.;
RT "Gene analysis of anticoagulation factors in Japanese thrombotic
RT patients. Genetic background of thrombophilia in Japan.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086851; BAC53631.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6475 MW; 3803696534BC9289 CRC64;

Query Match 63.0%; Score 126; DB 4; Length 55;
Best Local Similarity 67.6%; Pred. No. 1e-13;
Matches 25; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDT 37
DB 19 ANSFLKLRHSSLERECIEICDFEAKEIFQNVDDT 55

RESULT 6
Q63207 PRELIMINARY; PRT; 482 AA.
ID Q63207
AC Q63207;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

Q8J002
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Factor X.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96093366; PubMed=8578539;
RA Stanton C., Ross R.P., Hutson S., Wallin R.;
RT "Evidence for competition between vitamin K-dependent clotting factors
RT for intracellular processing by the vitamin K-dependent gamma-
RT carboxylase.";
RL Thromb. Res. 80:63-73(1995).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; X79807; CAAS6202.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001891; EGF_Ca.
DR InterPro; IPR001438; EGF_Ii.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR001254; Ser. protease Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS0240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN HIS; 1.
DR PROSITE; PS00135; TRYPSIN SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 56.5%; Score 113; DB 11; Length 482;
Best Local Similarity 43.2%; Pred. No. 1.7e-10;
Matches 19; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRCIXIXICDPXXAKXIFEDVDDTFLAFWSKH 44
DB 41 ANSFPEIKKGNLERECVBEICDFEAEVFEDEKTEFTFWNKY 84

RESULT 7
Q8JHC9 PRELIMINARY; PRT; 443 AA.
ID Q8JHC9
AC Q8JHC9;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Coagulation factor VIII.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Jagadeeswaran P.;
```


Db 41 ANSFFEFKGNLERECMEBICSEYEVREIFEDDEKTKYWTYKY 84

RESULT 10

Q99L32 PRELIMINARY; PRT; 481 AA.

AC Q99L32

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Coagulation factor X.

GN F10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RP Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RL Submitter: R.; to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; BC003877; AA003877.1; -.

DR HSSP; P00742; 1XKA.

DR MEROPS; S01.216; -.

DR MGD; MGI:103107; F10.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001254; Ser_protease_Try.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.

DR PRINTS; PRO0010; EGF_BLOOD.

DR PRINTS; PRO0001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp_SPC; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS02440; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW EGF-like domain; Hydrolase; Protease; Serine protease.

FT SIGNAL 1 40 POTENTIAL.

FT CHAIN 41 481 COAGULATION FACTOR X.

SQ SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;

Query Match 49.5%; Score 99; DB 11; Length 481;

Best Local Similarity 38.6%; Pred. No. 4e-08;

Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGLSLRXICXICDPXXAKXIFEDVDDTLAFWSKH 44

Db 41 ANSFFEFKGNLERECMEBICSEYEVREIFEDDEKTKYWTYKY 84

RESULT 11

O88947 PRELIMINARY; PRT; 481 AA.

AC O88947

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Coagulation factor X precursor.

GN F10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=C57BL6 X CBA; TISSUE=Liver;

RX MEDLINE=98347933; PubMed=9684791;

RA Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,

RA Castellino F.J., Rosen E.D.;

RT "Cloning and characterization of a cDNA encoding murine coagulation factor X.";

RL Thromb. Haemost. 80:87-91(1998).

RN [2] SEQUENCE FROM N.A.

RP STRAIN=1295J;

RC Cooper A., Liang Z., Castellino F.J., Rosen E.D.;

RT "Cloning and characterization of the Murine Factor X Gene.";

RL Thromb. Haemost. 0:0-0(2000).

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AF087644; AAC36345.1; -.

DR EMBL; AF211347; AAF22980.1; -.

DR HSSP; P00742; 1XKA.

DR MEROPS; S01.216; -.

DR MGD; MGI:103107; F10.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.

DR PRINTS; PRO0010; EGF_BLOOD.

DR PRINTS; PRO0001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp_SPC; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

DR PROSITE; PS02440; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW EGF-like domain; Hydrolase; Protease; Serine protease; Signal.

FT SIGNAL 1 40 POTENTIAL.

FT CHAIN 41 481 COAGULATION FACTOR X.

SQ SEQUENCE 481 AA; 54018 MW; 8AC09D5EF9D271E CRC64;

Query Match 49.5%; Score 99; DB 11; Length 481;

Best Local Similarity 38.6%; Pred. No. 4e-08;

Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANSFLXLRHGLSLRXICXICDPXXAKXIFEDVDDTLAFWSKH 44

Db 41 ANSFFEFKGNLERECMEBICSEYEVREIFEDDEKTKYWTYKY 84

RESULT 12

Q96PQ8 PRELIMINARY; PRT; 701 AA.

ID Q96PQ8

AC Q96PQ8

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Factor VII active site mutant immunoconjugate.

OS Homo sapiens (Human).

Search completed: December 30, 2003, 09:19:31
Job time : 36 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 09:17:31 ; Search time 21 Seconds
(without alignments)
88.651 Million cell updates/sec

Title: US09497591-1EDITED

Perfect score: 200

Sequence: 1 ANSFLXLRHGSLSRXCIIX.....XXAKXIFEDVDTLAFWSKH 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2.6/prodata/1/iaa/5A COMB.pcp.*

2: /cgn2.6/prodata/1/iaa/5B COMB.pcp.*

3: /cgn2.6/prodata/1/iaa/6A COMB.pcp.*

4: /cgn2.6/prodata/1/iaa/6B COMB.pcp.*

5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2.6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	176	88.0	44	3	US-08-955-636-19
2	174	87.0	44	3	US-08-955-636-24
3	174	87.0	44	3	US-08-955-636-35
4	168	84.0	44	3	US-08-955-636-1
5	168	84.0	44	3	US-08-955-636-20
6	168	84.0	44	3	US-08-955-636-21
7	168	84.0	44	3	US-08-955-636-25
8	168	84.0	45	2	US-08-965-832-2
9	168	84.0	419	1	US-08-955-411-1
10	168	84.0	419	1	US-08-955-471-1
11	168	84.0	419	4	US-09-667-570A-3
12	168	84.0	419	5	PCT-US92-10242-1
13	168	84.0	460	2	US-08-756-506-2
14	168	84.0	460	2	US-08-756-506-4
15	168	84.0	460	6	5270178-13
16	168	84.0	460	6	5270178-14
17	168	84.0	460	6	5270178-15
18	168	84.0	460	6	5270178-16
19	168	84.0	461	6	525537-2
20	168	84.0	461	6	525537-2
21	168	84.0	461	6	5270178-17
22	168	84.0	461	6	5270178-18
23	167	83.5	44	3	US-08-955-636-22
24	155	77.5	42	2	US-08-745-254A-2
25	155	77.5	461	6	5270178-2
26	151	75.5	41	1	US-08-229-280-5
27	137	68.5	410	3	US-09-065-872-1

28	137	68.5	410	4	US-09-667-570A-1	Sequence 1, Appli
29	129	64.5	409	3	US-09-065-872-2	Sequence 2, Appli
30	129	64.5	409	4	US-09-667-570A-2	Sequence 2, Appli
31	125	62.5	44	3	US-08-955-636-23	Sequence 23, Appli
32	115	57.5	44	3	US-08-955-636-2	Sequence 2, Appli
33	112	56.0	139	1	US-08-330-978-2	Sequence 2, Appli
34	112	56.0	139	1	US-08-474-042-2	Sequence 2, Appli
35	112	56.0	139	1	US-08-484-558-2	Sequence 2, Appli
36	112	56.0	139	1	US-08-774-592-2	Sequence 2, Appli
37	112	56.0	437	1	US-08-487-037-2	Sequence 2, Appli
38	112	56.0	437	1	US-08-487-037-3	Sequence 3, Appli
39	112	56.0	488	1	US-08-487-037-1	Sequence 1, Appli
40	109	54.5	487	1	US-08-469-486-53	Sequence 53, Appli
41	109	54.5	487	2	US-08-469-658-53	Sequence 53, Appli
42	109	54.5	492	1	US-08-469-486-2	Sequence 2, Appli
43	109	54.5	492	2	US-08-469-658-2	Sequence 2, Appli
44	108	54.0	448	1	US-08-295-411-3	Sequence 3, Appli
45	108	54.0	448	2	US-08-955-471-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-955-636-19
; Sequence 19, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-19

Query Match 88.0%; Score 176; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.6e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ANSFLXLRHGSLSRXCIIXICDFXXAKXIFEDVDTLAFWSKH 44
DB 1 ANSFLXLRHGSLSRXCIIXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 2
US-08-955-636-24
; Sequence 24, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-24

Query Match 87.0%; Score 174; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.5e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 3

US-08-955-636-35
; Sequence 35; Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-35

Query Match 87.0%; Score 174; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.5e-22;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 4

US-08-955-636-1
; Sequence 1; Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-1

Query Match 84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 93.2%; Pred. No. 3.5e-21;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFONVDDTLAFWSKH 44

RESULT 5

US-08-955-636-20
; Sequence 20; Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-20

Query Match 84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 6

US-08-955-636-21
; Sequence 21; Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-21

Query Match 84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXXLRHGSIXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

RESULT 7

US-08-955-636-25
; Sequence 25; Application US/08955636A
; Patent No. 6017882

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; GENERAL INFORMATION:
; APPLICANT: Nelsetuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid
US-08-955-636-25

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Query Match      84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ANSFLXLRHGSIXRCIXXICDXXKXKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRHSSIXRCIXXICDXXKXKXIFEDVDDTLAFWSKH 44

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RESULT 8
US-08-965-832-2
; Sequence 2, Application US/08965832
; Patent No. 5847085
; GENERAL INFORMATION:
; APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV
; TITLE OF INVENTION: Modified Protein C
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,832
; FILING DATE: 7-NOV-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,254
; FILING DATE: 8-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,768
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF 165/167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; FEATURE:
; NAME/KEY:
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
; OTHER INFORMATION: /note= "where Xaa means gamma
; OTHER INFORMATION: carboxylglutamic acid"
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2

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Query Match      84.0%; Score 168; DB 2; Length 45;
Best Local Similarity 93.2%; Pred. No. 3.6e-21;
Matches 41; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ANSFLXLRHGSIXRCIXXICDXXKXKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLXLRHSSIXRCIXXICDXXKXKXIFQNVDDTLAFWSKH 44

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RESULT 9
US-08-295-411-1
; Sequence 1, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffen, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESS: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..157
; OTHER INFORMATION: /note= "Protein C Light Chain"
; FEATURE:
; NAME/KEY: Region

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/ LOCATION: 158..169
/ OTHER INFORMATION: /note= "Protein C Activation
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 170..419
/ OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1

Query Match 84.0%; Score 168; DB 1; Length 419;
Best Local Similarity 72.7%; Pred. No. 4.4e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 ANSFLXXLRHGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 10
US-08-955-471-1
Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation

/ OTHER INFORMATION: Peptide"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 170..419
/ OTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-955-471-1

Query Match 84.0%; Score 168; DB 2; Length 419;
Best Local Similarity 72.7%; Pred. No. 4.4e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 ANSFLXXLRHGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 11
US-09-667-570A-3
Sequence 3, Application US/09667570A
Patent No. 6436397
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
FILE REFERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-570A-3

Query Match 84.0%; Score 168; DB 4; Length 419;
Best Local Similarity 72.7%; Pred. No. 4.4e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 1 ANSFLXXLRHGSIXRXCIXXICDPFXAKXIFEDVDDTLAFWSKH 44
Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 12
PCT-US92-10242-1
Sequence 1, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242

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/
/ FILING DATE: 19921118
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR0472P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 419 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..157
/ OTHER INFORMATION: /note= "Protein C Light Chain"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 158..169
/ OTHER INFORMATION: /note= "Protein C Activation"
/ OTHER INFORMATION: Peptide"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 170..419
/ OTHER INFORMATION: /note= "Protein C Heavy Chain"
PCT-US92-10242-1

Query Match 84.0%; Score 168; DB 5; Length 419;
Best Local Similarity 72.7%; Pred. No. 4.4e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANSFLXLRHSGSLXRCIXXICDPXXAXXIFEDVDDTLAFWSKH 44
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DB 1 ANSFLFLRHSLRECEIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 13
US-08-756-506-2
; Sequence 2, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 95-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 460 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-506-4

Query Match 84.0%; Score 168; DB 2; Length 460;
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Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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DB 43 ANSFLFLRHSLRECEIEICDFEAKEIFQNVDDTLAFWSKH 86

RESULT 14
US-08-756-506-4
; Sequence 4, Application US/08756506
; Patent No. 5905185
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Cottingham, Ian R.
; APPLICANT: Temperley, Simon M.
; APPLICANT: Foster, Donald C.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prunkard, Donna E.
; TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,506
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 95-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 460 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-506-4

Query Match 84.0%; Score 168; DB 2; Length 460;
Best Local Similarity 72.7%; Pred. No. 4.9e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
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RESULT 15
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 ; Patent No. 5270178
 ; APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
 ; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
 ; ZYMOGEN FORMS OF HUMAN PROTEIN C
 ; NUMBER OF SEQUENCES: 21
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/484,133
 ; FILING DATE: 23-FEB-1990
 ; SEQ ID NO:13:
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Search completed: December 30, 2003, 09:20:38
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2003, 09:19:36 ; Search time 31 Seconds
(without alignments)
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Perfect score: 200

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Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	91.0	419	12	US-10-168-407-3 Sequence 3, Appli
2	182	91.0	419	12	US-10-168-407-4 Sequence 4, Appli
3	182	91.0	419	15	US-10-182-263-3 Sequence 3, Appli
4	182	91.0	419	15	US-10-182-263-4 Sequence 4, Appli
5	182	91.0	419	15	US-10-182-263-5 Sequence 5, Appli
6	174	87.0	419	12	US-10-168-407-5 Sequence 5, Appli
7	174	87.0	419	12	US-10-168-407-6 Sequence 6, Appli
8	174	87.0	419	15	US-10-182-263-6 Sequence 6, Appli
9	168	84.0	44	15	US-10-298-330-1 Sequence 1, Appli
10	168	84.0	419	11	US-09-978-917A-4 Sequence 4, Appli
11	168	84.0	419	12	US-10-168-407-1 Sequence 1, Appli
12	168	84.0	419	15	US-10-182-263-1 Sequence 1, Appli
13	168	84.0	461	11	US-09-978-917A-2 Sequence 2, Appli
14	168	84.0	461	12	US-10-168-407-2 Sequence 2, Appli
15	168	84.0	461	15	US-10-182-263-2 Sequence 2, Appli

16	115	57.5	44	15	US-10-298-330-2	Sequence 2, Appli
17	108	54.0	488	12	US-10-348-504-44	Sequence 44, Appli
18	108	54.0	488	12	US-10-407-123-27	Sequence 27, Appli
19	101	50.5	44	15	US-10-298-330-18	Sequence 18, Appli
20	98	49.0	406	11	US-03-782-587B-3	Sequence 3, Appli
21	98	49.0	466	12	US-10-375-741-14	Sequence 14, Appli
22	98	49.0	466	15	US-10-017-122-2	Sequence 2, Appli
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25	95	47.5	406	12	US-10-386-898-7	Sequence 7, Appli
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32	84	42.0	40	15	US-10-298-330-25	Sequence 25, Appli
33	84	42.0	96	11	US-09-759-130B-313	Sequence 313, App
34	84	42.0	96	12	US-10-188-495-43	Sequence 43, Appli
35	84	42.0	96	15	US-10-189-123-43	Sequence 43, Appli
36	84	42.0	209	11	US-09-759-130B-312	Sequence 312, App
37	84	42.0	209	12	US-10-188-495-42	Sequence 42, Appli
38	84	42.0	209	15	US-10-189-123-42	Sequence 42, Appli
39	84	42.0	226	11	US-09-759-130B-310	Sequence 310, App
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41	84	42.0	226	15	US-10-189-123-40	Sequence 40, Appli
42	82	41.0	40	15	US-10-298-330-24	Sequence 24, Appli
43	82	41.0	622	15	US-10-020-141-8	Sequence 8, Appli
44	82	41.0	622	15	US-10-017-631-2	Sequence 2, Appli
45	82	41.0	622	15	US-10-214-932-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-10-168-407-3
; Sequence 3, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Garlitz, Bruce E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-3

Query Match 91.0%; Score 182; DB 12; Length 419;
Best Local Similarity 79.5%; Pred. No. 3.2e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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DB 1 ANSFLXLRHSGSLXRCIXXICDFXXAKXIFEDVDTLAFWSKH 44

RESULT 2

US-10-168-407-4
; Sequence 4, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Garlitz, Bruce E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407

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; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-4

Query Match          91.0%; Score 182; DB 12; Length 419;
Best Local Similarity 79.5%; Pred. No. 3.2e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 3
US-10-182-263-3
; Sequence 3, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3

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Best Local Similarity 79.5%; Pred. No. 3.2e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 4
US-10-182-263-4
; Sequence 4, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-5

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Best Local Similarity 77.3%; Pred. No. 7.1e-21;
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RESULT 5
US-10-182-263-5
; Sequence 5, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-5

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Best Local Similarity 79.5%; Pred. No. 3.2e-22;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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; Sequence 5, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan W
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-5

Query Match          87.0%; Score 174; DB 12; Length 419;
Best Local Similarity 77.3%; Pred. No. 7.1e-21;
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RESULT 7
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RESULT 12

US-10-182-263-1

; Sequence 1, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; PRIOR FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-1

Query Match 84.0%; Score 168; DB 15; Length 419;
Best Local Similarity 72.7%; Pred. No. 7.3e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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Db 1 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 44

RESULT 13

US-09-978-917A-2

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; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978, 917A
; CURRENT FILING DATE: 2001-10-17
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; LOCATION: (43)...(461)
US-09-978-917A-2

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; Sequence 2, Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-2

Query Match 84.0%; Score 168; DB 12; Length 461;
Best Local Similarity 72.7%; Pred. No. 8.1e-20;
Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinnell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2

Query Match 84.0%; Score 168; DB 15; Length 461;
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Matches 32; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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Db 43 ANSFLELRHSSLERECIEICDFEAKEIFQNVDDTLAFWSKH 86

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